IN THE CLAIMS

This listing of the claims will replace all prior versions, and listings, of the claims in the application.

1 – 5. (Cancelled)

6. (Currently amended) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase mutated with respect to a wild-type cellobiohydrolase represented by SEQ ID NO: 99 [[5]], the mutation providing means for improving cellobiohydrolase functionality with respect to the wild-type cellobiohydrolase functionality, wherein the functionality is thermostability, enzymatic activity, catalytic activity, product inhibition, glycosylation, and/or peptide strain.

7. (Previously presented) The nucleic acid molecule of claim 6 wherein the functionality is thermostability and the means for improving comprises proline substituted at position 8.

8. (Cancelled)

9. (Previously presented) The nucleic acid molecule of claim 7 wherein the means for improving further comprises the helix-capping mutation defined as an arginine or aspartic acid residue substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410, and any combination thereof.

10. (Previously presented) The nucleic acid molecule of claim 7 wherein the means for improving further comprises substitution of glycine at position 99.

11. (Currently amended) A method for mutating a nucleic acid encoding a wild type cellobiohydrolase of SEQ ID NO: 99 [[5]], the method comprising mutating the wild type cellobiohydrolase with proline substituted at position 8.

12. (Previously presented) The method of claim 11, wherein the mutation further comprises substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384, and any combination thereof.

13. (Previously presented) The method of claim 11, wherein the step of mutating comprises site-directed mutagenesis.

14. (Currently amended) The method of claim 11, further comprising a step of shortening a linker region of the wild-type cellobiohydrolase with respect to wild-type linker region SEQ ID NO: 2 to provide a linker region having a length of from about 6 amino acids to about 17 amino acids located between a catalytic domain and a cellulose binding domain (CBD) of SEQ ID NO: 99 [[5]].

15. – 19. (Cancelled)

20. (Previously presented) The nucleic acid molecule of claim 7 wherein the functionality is thermostability and the means for improving further comprises substitution of a cysteine at positions 197 and 370.

21. (Previously presented) The nucleic acid molecule of claim 7 wherein the functionality is thermostability and the means for improving further comprises substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384, and any combination thereof.

22. (Previously presented) The nucleic acid molecule of claim 7 wherein the functionality is thermostability and the means for improving further comprises substitution of an alanine at a position selected from the group consisting of position 45, 270, 384, and any combination thereof.

23. (Cancelled)

24. (Cancelled)

25. (Currently amended) The nucleic acid molecule of claim 6, wherein the variant cellobiohydrolase comprises a linker region having a length of from about 6 amino acids to about 17 amino acids located between a catalytic domain and a cellulose binding domain (CBD) and wherein the variant cellobiohydrolase comprises a proline substituted at position 8 relative to SEQ ID NO: 99 [[5]].

26. (Currently amended) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase mutated with respect to a wild-type cellobiohydrolase of SEQ ID NO: 99 [[5]], the mutation comprising proline substituted in the place of the serine at position 8.

27. - 28. (Cancelled)

29. (Previously presented) The nucleic acid molecule of claim 6 wherein the means for improving functionality comprises means for enhancing thermostability.

30. (Currently amended) The nucleic acid molecule of claim 26, wherein the variant cellobiohydrolase is further mutated with a mutation selected from the group consisting of:

(a) proline substituted at a position selected from the group consisting of position [[9,]] 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;

(b) a helix-capping mutation defined as an arginine or aspartic acid residue substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;

(c) substitution of glycine at position 99;

(d) substitution of cysteine at positions 197 and 370;

(e) substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 684 and any combination thereof,

(f) alanine substitution at a position selected from the group consisting of position 45, 270, 384 and any combination thereof; and

(g) any combination of the mutations of (a), (b), (c), (d), (e), (f),

wherein the positional reference is within the amino acid sequence of the wild-type cellobiohydrolase SEQ ID NO: 99 [[5]].

31. (Currently amended) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase mutated with respect to a wild-type cellobiohydrolase represented by SEQ ID NO: 99 [[5]], wherein the mutation comprises a proline substituted at position 8, and wherein the proline substitution improves the functionality of the variant cellobiohydrolase with respect to the wild-type cellobiohydrolase by improving thermostability.

32. (Previously presented) The nucleic acid molecule of claim 31 wherein the mutation further comprises an arginine or aspartic acid residue substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410, and any combination thereof.

33. (Previously presented) The nucleic acid molecule of claim 31 wherein the mutation further comprises substitution of glycine at position 99.

34. (Previously presented) The nucleic acid molecule of claim 31 wherein the mutation further comprises substitution of a cysteine at positions 197 and 370.

35. (Previously presented) The nucleic acid molecule of claim 31 wherein the mutation further comprises substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384, and any combination thereof.